A1 SUB B1

This application is a divisional of U.S. Application No. 09/019,160, filed February 6, 1998, now US patent No. 6306,598; which claims priority to U.S. Provisional Application No. 60/037,393, filed February 7, 1997, and to U.S. Provisional Application No. 60/070,562, filed January 6, 1998, the disclosures of which are fully incorporated herein by reference.

Substitute the fourth full paragraph on page 18 (appearing at lines 14-15) with the following paragraph:

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FIGURES 10A-D are composites of a electropherogram gel scan of PCR amplifications at D16S405 and D16S401 loci.

Substitute the fifth full paragraph on page 18 (appearing at lines 16-17) with the following paragraph:

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FIGURES 11A-B are composites of a electropherogram gel scan of PCR amplifications at D16S401 locus.

Substitute the sixth full paragraph on page 18 (appearing at lines 18-19) with the following paragraph:

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FIGURES 12A-F are composites of a electropherogram gel scan of PCR amplifications at D15S127 and D15S153 loci.

Substitute the seventh full paragraph on page 18 (appearing at lines 20-21) with the following paragraph:

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FIGURES 13A-C are composites of a electropherogram gel scan of PCR amplifications at D16S401 locus.

Substitute the second full paragraph on page 86 (appearing at lines 12-22) with the following paragraph:

Figure 9 shows two examples of electropherogram gel scans, aligned by PCR product size, comparing the PCR products obtained with *Taq* and *Tne* polymerases with a 10-minute final extension. For the D15S153 locus, *Taq* exhibited non-templated nucleotide addition to 40% of the PCR product (Figure 9A), while *Tne* exhibited no such addition of non-templated nucleotides (Figure 9B). Similar results were obtained with the D15S127 locus: 53% of the *Taq* PCR products demonstrated non-templated nucleotide addition (Figure 9C), while none of the *Tne* PCR products demonstrated non-templated nucleotide addition (Figure 9D). These results demonstrate the difficulty in identifying alleles in a heterogeneous pattern as generated by *Taq* amplification, compared to the more homogeneous, simple pattern generated by amplification with *Tne*.

A6

Substitute the second full paragraph on page 87 (appearing at lines 11-21) with the following paragraph:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95°C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72°C; 10min final extension at 72°C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 7 summarizes the results obtained. Examples of the electropherogram data are shown in Figures 10A-D.

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Substitute the second full paragraph on page 88 (appearing at lines 11-21) with the following paragraph:

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Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95°C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72°C; 10min final extension at 72°C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 8 summarizes the results obtained. An example of the electropherogram data are shown in Figures 11A-B.

Substitute the second full paragraph on page 90 (appearing at lines 12-22) with the following paragraph:

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Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 10min final extension at 72 °C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 9 summarizes the results obtained. Examples of the electropherogram data are shown in Figures 12A-F.

Substitute the second full paragraph on page 91 (appearing at lines 15-25) with the following paragraph:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 10min final extension at 72 °C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Heights of the n and n+1 peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 10 summarizes the results obtained. An example of the electropherogram data are shown in Figures 13A-C.

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In the Claims:

Please cancel claims 38 and 43-51, without prejudice to or disclaimer of the subject matter contained therein.